

2007-11-05 [58049-00003] sequence listing_ST25
SEQUENCE LISTING

<110> Mogam Biotechnology Research Institute
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Kim, Jang Seong
Jang, Jihoon
Yum, Jungsun
Chung, Soo-il

<120> Novel Detoxified Mutants of Escherichia coli Heat-Labile
Enterotoxin

<130> 58049-00003

<140> US 10/088,202

<141> 2002-03-15

<150> PCT/KR99/00555

<151> 1999-09-15

<160> 6

<170> PatentIn version 3.4

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<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<220>

<221> primer_bind

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<223> Primer

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<213> Escherichia coli

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<221> SIGNAL

<222> (1)..(18)

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Tyr Ala Asn Gly Asp Arg Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp
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Glu Ile Lys Arg Ser Gly Gly Leu Met Pro Arg Gly His Asn Glu Tyr
 35 40 45

Phe Asp Arg Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg
 50 55 60

Gly Thr Gln Thr Gly Phe Val Arg Tyr Asp Asp Gly Tyr Val Ser Thr
 65 70 75 80

Tyr Leu Ser Leu Arg Ser Ala His Leu Ala Gly Gln Ser Ile Leu Ser
 85 90 95

Gly Tyr Ser Thr Tyr Tyr Ile Tyr Val Ile Ala Thr Ala Pro Asn Met
 100 105 110

Phe Asn Val Asn Asp Val Leu Gly Val Tyr Ser Pro His Pro Tyr Glu
 115 120 125

Gln Glu Val Ser Ala Leu Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly
 130 135 140

Trp Tyr Arg Val Asn Phe Gly Val Ile Asp Glu Arg Leu His Arg Asn
 145 150 155 160

Arg Glu Tyr Arg Asp Arg Tyr Tyr Arg Asn Leu Asn Ile Ala Pro Ala
 165 170 175

Glu Asp Gly Tyr Arg Leu Ala Gly Phe Pro Pro Asp His Gln Ala Trp
 180 185 190

Arg Glu Glu Pro Trp Ile His His Ala Pro Gln Gly Cys Gly Asn Ser
 195 200 205

Ser Arg Thr Ile Thr Gly Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu
 210 215 220

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Ser Thr Ile Tyr Leu Arg Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile
225 230 235 240

Phe Ser Asp Tyr Gln Ser Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp
245 250 255

Glu Leu Met Asn Lys Val Lys Phe Tyr Val Leu Phe Thr Ala Leu Leu
260 265 270

Ser Ser Leu Cys Ala His Gly Ala Pro Gln Ser Ile Thr Glu Leu Cys
275 280 285

Ser Glu Tyr His Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys Ile Leu
290 295 300

Ser Tyr Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile Ile Thr
305 310 315 320

Phe Lys Ser Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln His
325 330 335

Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg
340 345 350

Ile Thr Tyr Leu Thr Glu Thr Lys Ile Asp Lys Leu Cys Val Trp Asn
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Asn Lys Thr Pro Asn Ser Ile Ala Ala Ile Ser Met Glu Asn
370 375 380

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<212> DNA
<213> Escherichia coli

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tgctcactta gcaggacagt ctatattatc aggatattcc acttactata tatatgttat 480
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gtattacaga aatctgaata tagctccggc agaggatggt tacagattag caggtttccc    720
accggatcac caagcttgga gagaagaacc ctggattcat catgcaccac aaggttgttg    780
aaattcatca agaacaatca caggtgatac ttgtaatgag gagaccocaga atctgagcac    840
aatatatctc agggaatatc aatcaaaaagt taagaggcag atatttttcag actatcagtc    900
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<210> 5
<211> 380
<212> PRT
<213> Escherichia coli

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<220>
<221> SIGNAL
<222> (1)..(18)

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<400> 5

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Met Lys Asn Ile Thr Phe Ile Phe Phe Ile Leu Leu Ala Ser Pro Leu
1           5           10          15

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Tyr Ala Asn Gly Asp Arg Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp
20           25           30

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Glu Ile Lys Arg Ser Gly Gly Leu Met Pro Arg Gly His Asn Glu Tyr
35           40           45

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Phe Asp Arg Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg
50           55           60

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Gly Thr Gln Thr Gly Phe Val Arg Tyr Asp Asp Gly Tyr Val Ser Thr
65 70 75 80

Ser Leu Ser Leu Arg Ser Ala His Leu Ala Gly Gln Ser Ile Leu Ser
85 90 95

Gly Tyr Ser Thr Tyr Tyr Ile Tyr Val Ile Ala Thr Ala Pro Asn Met
100 105 110

Phe Asn Val Asn Asp Val Leu Gly Val Tyr Ser Pro His Pro Tyr Gln
115 120 125

Val Ser Ala Leu Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr
130 135 140

Arg Val Asn Phe Gly Val Ile Asp Glu Arg Leu His Arg Asn Arg Glu
145 150 155 160

Tyr Arg Asp Arg Tyr Tyr Arg Asn Leu Asn Ile Ala Pro Ala Glu Asp
165 170 175

Gly Tyr Arg Leu Ala Gly Phe Pro Pro Asp His Gln Ala Trp Arg Glu
180 185 190

Glu Pro Trp Ile His His Ala Pro Gln Gly Cys Gly Asn Ser Ser Arg
195 200 205

Thr Ile Thr Gly Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu Ser Thr
210 215 220

Ile Tyr Leu Arg Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser
225 230 235 240

Asp Tyr Gln Ser Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp Glu Leu
245 250 255

Met Asn Lys Val Lys Phe Tyr Val Leu Phe Thr Ala Leu Leu Ser Ser
260 265 270

Leu Cys Ala His Gly Ala Pro Gln Ser Ile Thr Glu Leu Cys Ser Glu
275 280 285

Tyr His Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys Ile Leu Ser Tyr
290 295 300

Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile Ile Thr Phe Lys
305 310 315 320

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Ser Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp
325 330 335

Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Thr
340 345 350

Tyr Leu Thr Glu Thr Lys Ile Asp Lys Leu Cys Val Trp Asn Asn Lys
355 360 365

Thr Pro Asn Ser Ile Ala Ala Ile Ser Met Glu Asn
370 375 380

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catttttttt attttattag catcgccatt atatgcaaat ggcgacagat tataccgtgc 240
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